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RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/10/067,615

TIME: 13:19:32

Input Set : A:\432d1.app.txt

Output Set: N:\CRF3\02262002\J067615.raw

3 <110> APPLICANT: Alnemri, Emad S.
 5 <120> TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
 6 METHODS OF USE THEREOF
 8 <130> FILE REFERENCE: 480140.432D1
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/067,615
 11 <141> CURRENT FILING DATE: 2002-02-04
 13 <160> NUMBER OF SEQ ID NOS: 6
 15 <170> SOFTWARE: PatentIn Ver. 2.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1236
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (1)..(1233)
 26 <400> SEQUENCE: 1
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 29 1 5 10 15
 31 agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ctc 96
 32 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
 33 20 25 30
 35 cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg 144
 36 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
 37 35 40 45
 39 gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag 192
 40 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
 41 50 55 60
 43 cag aga gtg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg 240
 44 Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 45 65 70 75 80
 47 tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc 288
 48 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
 49 85 90 95
 51 tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc 336
 52 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
 53 100 105 110
 55 tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccc 384
 56 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
 57 115 120 125
 59 tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc acc ttc 432
 60 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
 61 130 135 140

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63	cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca ggg tgt	480
64	Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys	
65	145 150 155 160	
67	ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt gac atc	528
68	Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile	
69	165 170 175	
71	gaa tgt gtc cac aaa gaa tca ggc atc atc ata gga gtc aca gtt gca	576
72	Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala	
73	180 185 190	
75	gcc gta gtc ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg	624
76	Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp	
77	195 200 205	
79	aag aaa gtc ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg	672
80	Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly	
81	210 215 220	
83	gac cct gag cgt gtg gac aga agc tca caa cga cct ggg gct gag gac	720
84	Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp	
85	225 230 235 240	
87	aat gtc ctc aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct	768
88	Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro	
89	245 250 255	
91	gag cag gaa atg gaa gtc cag gag cca gca gag cca aca ggt gtc aac	816
92	Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn	
93	260 265 270	
95	atg ttg tcc ccc ggg gag tca gag cat ctg ctg gaa ccg gca gaa gct	864
96	Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala	
97	275 280 285	
99	gaa agg tct cag agg agg agg ctg ctg gtt cca gca aat gaa ggt gat	912
100	Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp	
101	290 295 300	
103	ccc act gag act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg	960
104	Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val	
105	305 310 315 320	
107	ccc ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac	1008
108	Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp	
109	325 330 335	
111	aat gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc	1056
112	Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr	
113	340 345 350	
115	ttg tac acg atg ctg ata aag tgg gtc aac aaa acc ggg cga gat gcc	1104
116	Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala	
117	355 360 365	
119	tct gtc cac acc ctg ctg gat gcc ttg gag acg ctg gga gag aga ctt	1152
120	Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu	
121	370 375 380	
123	gcc aag cag aag att gag gac cac ttg ttg agc tct gga aag ttc atg	1200
124	Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met	
125	385 390 395 400	
127	tat cta gaa ggt aat gca gac tct gcc atg tcc taa	1236

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128 Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
129           405                      410
132 <210> SEQ ID NO: 2
133 <211> LENGTH: 411
134 <212> TYPE: PRT
135 <213> ORGANISM: Homo sapiens
137 <400> SEQUENCE: 2
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139   1           5           10           15
141 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
142           20           25           30
144 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
145           35           40           45
147 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
148           50           55           60
150 Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
151   65           70           75           80
153 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
154           85           90           95
156 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
157           100          105          110
159 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
160           115          120          125
162 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
163           130          135          140
165 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
166 145           150          155          160
168 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
169           165          170          175
171 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
172           180          185          190
174 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
175           195          200          205
177 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
178           210          215          220
180 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
181 225           230          235          240
183 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
184           245          250          255
186 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
187           260          265          270
189 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
190           275          280          285
192 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
193           290          295          300
195 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
196 305           310          315          320
198 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
199           325          330          335

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201 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
202           340           345           350
204 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
205           355           360           365
207 Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
208           370           375           380
210 Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
211 385           390           395           400
213 Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
214           405           410
217 <210> SEQ ID NO: 3
218 <211> LENGTH: 900
219 <212> TYPE: DNA
220 <213> ORGANISM: Homo sapiens
222 <220> FEATURE:
223 <221> NAME/KEY: CDS
224 <222> LOCATION: (1)..(897)
226 <400> SEQUENCE: 3
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228 Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp
229 1           5           10           15
231 aga gcg ccc cgg ccg cct gat ggc cga ggc agg gtg cga ccc agg acc 96
232 Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
233           20           25           30
235 caa gac ggc gtc ggg aac cat acc atg gcc cgg atc ccc aag acc cta 144
236 Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro Lys Thr Leu
237           35           40           45
239 aag ttc gtc gtc gtc atc gtc gcg gtc ctg ctg cca gtc cta gct tac 192
240 Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr
241           50           55           60
243 tct gcc acc act gcc cgg cag gag gaa gtt ccc cag cag aca gtg gcc 240
244 Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
245 65           70           75           80
247 cca cag caa cag agg cac agc ttc aag ggg gag gag tgt cca gca gga 288
248 Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly
249           85           90           95
251 tct cat aga tca gaa cat act gga gcc tgt aac ccg tgc aca gag ggt 336
252 Ser His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
253           100          105          110
255 gtg gat tac acc aac gct tcc aac aat gaa cct tct tgc ttc cca tgt 384
256 Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys
257           115          120          125
259 aca gtt tgt aaa tca gat caa aaa cat aaa agt tcc tgc acc atg acc 432
260 Thr Val Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr
261           130          135          140
263 aga gac aca gtg tgt cag tgt aaa gaa ggc acc ttc cgg aat gaa aac 480
264 Arg Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
265 145          150          155          160
267 tcc cca gag atg tgc cgg aag tgt agc agg tgc cct agt ggg gaa gtc 528

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268 Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val
269          165          170          175
271 caa gtc agt aat tgt acg tcc tgg gat gat atc cag tgt gtt gaa gaa 576
272 Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu
273          180          185          190
275 ttt ggt gcc aat gcc act gtg gaa acc cca gct gct gaa gag aca atg 624
276 Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met
277          195          200          205
279 aac acc agc ccg ggg act cct gcc cca gct gct gaa gag aca atg aac 672
280 Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn
281          210          215          220
283 acc agc cca ggg act cct gcc cca gct gct gaa gag aca atg acc acc 720
284 Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
285 225          230          235          240
287 agc ccg ggg act cct gcc cca gct gct gaa gag aca atg acc acc agc 768
288 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser
289          245          250          255
291 ccg ggg act cct gcc cca gct gct gaa gag aca atg acc acc agc ccg 816
292 Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro
293          260          265          270
295 ggg act cct gcc tct tct cat tac ctc tca tgc acc atc gta ggg atc 864
296 Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
297          275          280          285
299 ata gtt cta att gtg ctt ctg att gtg ttt gtt tga 900
300 Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
301          290          295
304 <210> SEQ ID NO: 4
305 <211> LENGTH: 299
306 <212> TYPE: PRT
307 <213> ORGANISM: Homo sapiens
309 <400> SEQUENCE: 4
310 Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp
311 1          5          10          15
313 Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
314          20          25          30
316 Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro Lys Thr Leu
317          35          40          45
319 Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr
320          50          55          60
322 Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
323 65          70          75          80
325 Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly
326          85          90          95
328 Ser His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
329          100          105          110
331 Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys
332          115          120          125
334 Thr Val Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr
335          130          135          140

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Wrong Format